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RAW SEQUENCE LISTING

DATE: 04/08/2002

PATENT APPLICATION: US/09/782,587B

TIME: 16:03:58

Input Set : A:\0213us310-SEQUENCE_LISTING-Nov2001.txt

Output Set: N:\CRF3\04082002\I782587B.raw

ENTERED

3 <110> APPLICANT: PEDERSEN, ANDERS H.
 4 ANDERSON, KIM V.
 5 BORNAES, CLAUS
 7 <120> TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
 9 <130> FILE REFERENCE: 31-001100US
 11 <140> CURRENT APPLICATION NUMBER: 09/782,587B
 12 <141> CURRENT FILING DATE: 2002-03-26
 14 <150> PRIOR APPLICATION NUMBER: PA 2000 00218
 15 <151> PRIOR FILING DATE: 2000-02-11
 17 <150> PRIOR APPLICATION NUMBER: 60/184,036
 18 <151> PRIOR FILING DATE: 2000-02-22
 20 <150> PRIOR APPLICATION NUMBER: 60/241,916
 21 <151> PRIOR FILING DATE: 2000-10-18
 23 <160> NUMBER OF SEQ ID NOS: 19
 25 <170> SOFTWARE: PatentIn Ver. 2.1
 27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 406
 29 <212> TYPE: PRT
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 33 <221> NAME/KEY: MOD_RES
 34 <222> LOCATION: (6)..(7)
 35 <223> OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
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 39 <222> LOCATION: (14)
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 54 <222> LOCATION: (25)..(26)
 55 <223> OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
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 59 <222> LOCATION: (29)
 60 <223> OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid

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62 <220> FEATURE:

63 <221> NAME/KEY: MOD_RES

64 <222> LOCATION: (35)

65 <223> OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid

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72 20 25 30
W--> 74 Asp Ala Xaa Arg Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp
75 35 40 45
77 Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln
78 50 55 60
80 Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn
81 65 70 75 80
83 Cys Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly
84 85 90 95
86 Gly Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys
87 100 105 110
89 Arg Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr
90 115 120 125
92 Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg
93 130 135 140
95 Asn Ala Ser Lys Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro
96 145 150 155 160
98 Lys Gly Glu Cys Pro Trp Gln Val Leu Leu Val Asn Gly Ala Gln
99 165 170 175
101 Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala
102 180 185 190
104 His Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu
105 195 200 205
107 Gly Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg
108 210 215 220
110 Val Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn
111 225 230 235 240
113 His Asp Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp
114 245 250 255
116 His Val Val Pro Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr
117 260 265 270
119 Leu Ala Phe Val Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu
120 275 280 285
122 Asp Arg Gly Ala Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg
123 290 295 300
125 Leu Met Thr Gln Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp Ser
126 305 310 315 320
128 Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser
129 325 330 335
131 Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr
132 340 345 350

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134 Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys
135          355          360          365
137 Ala Thr Val Gly His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile
138          370          375          380
140 Glu Trp Leu Gln Lys Leu Met Arg Ser Glu Pro Arg Pro Gly Val Leu
141 385          390          395          400
143 Leu Arg Ala Pro Phe Pro
144          405
147 <210> SEQ ID NO: 2
148 <211> LENGTH: 1338
149 <212> TYPE: DNA
150 <213> ORGANISM: Homo sapiens
152 <220> FEATURE:
153 <221> NAME/KEY: CDS
154 <222> LOCATION: (115)..(1332)
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160                                     Ala
161                                     1
163 aat gcc ttt ctg gaa gag ctc cgc cct ggc tcc ctg gaa cgc gaa tgc 165
164 Asn Ala Phe Leu Glu Glu Leu Arg Pro Gly Ser Leu Glu Arg Glu Cys
165          5          10          15
167 aaa gag gaa cag tgc agc ttt gag gaa gcc cgg gag att ttc aaa gac 213
168 Lys Glu Glu Gln Cys Ser Phe Glu Glu Ala Arg Glu Ile Phe Lys Asp
169          20          25          30
171 gct gag cgg acc aaa ctg ttt tgg att agc tat agc gat ggc gat cag 261
172 Ala Glu Arg Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp Gln
173          35          40          45
175 tgc gcc tcc agc cct tgc cag aac ggg ggc tcc tgc aaa gac cag ctg 309
176 Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln Leu
177 50          55          60          65
179 cag agc tat atc tgc ttc tgc ctg cct gcc ttt gag ggg cgc aat tgc 357
180 Gln Ser Tyr Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn Cys
181          70          75          80
183 gaa acc cat aag gat gac cag ctg att tgc gtc aac gaa aac ggg ggc 405
184 Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly Gly
185          85          90          95
187 tgc gag cag tac tgc agc gat cac acg ggc acg aag cgg agc tgc cgc 453
188 Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys Arg
189          100          105          110
191 tgc cac gaa ggc tat agc ctc ctg gct gac ggg gtg tcc tgc acg ccc 501
192 Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr Pro
193          115          120          125
195 acg gtg gaa tac cct tgc ggg aag att ccc att cta gaa aag cgg aac 549
196 Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg Asn
197 130          135          140          145
199 gct agc aaa ccc cag ggc cgg atc gtc ggc ggg aag gtc tgc cct aag 597
200 Ala Ser Lys Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro Lys

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201		150		155		160	
203	ggg gag tgc ccc tgg cag gtc ctg ctc ctg gtc aac ggg gcc cag ctg	645					
204	Gly Glu Cys Pro Trp Gln Val Leu Leu Leu Val Asn Gly Ala Gln Leu						
205		165		170		175	
207	tgc ggc ggg acc ctc atc aat acc att tgg gtc gtg tcc gcc gct cac	693					
208	Cys Gly Gly Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala His						
209		180		185		190	
211	tgc ttc gat aag att aag aat tgg cgg aac ctc atc gct gtg ctc ggc	741					
212	Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu Gly						
213		195		200		205	
215	gaa cac gat ctg tcc gag cat gac ggg gac gaa cag tcc cgc cgg gtg	789					
216	Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg Val						
217	210		215		220		225
219	gct cag gtc atc att ccc tcc acc tat gtg cct ggc acg acc aat cac	837					
220	Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn His						
221		230		235		240	
223	gat atc gct ctg ctc cgc ctc cac cag ccc gtc gtg ctc acc gat cac	885					
224	Asp Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp His						
225		245		250		255	
227	gtc gtg cct ctg tgc ctg cct gag cgg acc ttt agc gaa cgc acg ctg	933					
228	Val Val Pro Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr Leu						
229		260		265		270	
231	gct ttc gtc cgc ttt agc ctc gtg tcc ggc tgg ggc cag ctg ctc gac	981					
232	Ala Phe Val Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu Asp						
233		275		280		285	
235	cgg ggc gct acc gct ctc gag ctg atg gtg ctc aac gtc ccc cgg ctg	1029					
236	Arg Gly Ala Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg Leu						
237	290		295		300		305
239	atg acc cag gac tgc ctg cag cag tcc cgc aaa gtg ggg gac tcc ccc	1077					
240	Met Thr Gln Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp Ser Pro						
241		310		315		320	
243	aat atc acg gag tat atg ttt tgc gct ggc tat agc gat ggc tcc aag	1125					
244	Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser Lys						
245		325		330		335	
247	gat agc tgc aag ggg gac tcc ggc ggg ccc cat gcc acg cac tat cgc	1173					
248	Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr Arg						
249		340		345		350	
251	ggg acc tgg tac ctc acc ggg atc gtc agc tgg ggc cag ggc tgc gcc	1221					
252	Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys Ala						
253		355		360		365	
255	acg gtg ggg cac ttt ggc gtc tac acg cgc gtc agc cag tac att gag	1269					
256	Thr Val Gly His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile Glu						
257	370		375		380		385
259	tgg ctg cag aag ctc atg cgg agc gaa ccc cgg ccc ggg gtg ctc ctg	1317					
260	Trp Leu Gln Lys Leu Met Arg Ser Glu Pro Arg Pro Gly Val Leu Leu						
261		390		395		400	
263	cgg gcc cct ttc cct tgataa	1338					
264	Arg Ala Pro Phe Pro						
265		405					

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268 <210> SEQ ID NO: 3
269 <211> LENGTH: 406
270 <212> TYPE: PRT
271 <213> ORGANISM: Homo sapiens
273 <400> SEQUENCE: 3
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277 Cys Lys Glu Glu Gln Cys Ser Phe Glu Ala Arg Glu Ile Phe Lys
278 20 25 30
280 Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp
281 35 40 45
283 Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln
284 50 55 60
286 Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn
287 65 70 75 80
289 Cys Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly
290 85 90 95
292 Gly Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys
293 100 105 110
295 Arg Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr
296 115 120 125
298 Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg
299 130 135 140
301 Asn Ala Ser Lys Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro
302 145 150 155 160
304 Lys Gly Glu Cys Pro Trp Gln Val Leu Leu Val Asn Gly Ala Gln
305 165 170 175
307 Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala
308 180 185 190
310 His Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu
311 195 200 205
313 Gly Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg
314 210 215 220
316 Val Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn
317 225 230 235 240
319 His Asp Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp
320 245 250 255
322 His Val Val Pro Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr
323 260 265 270
325 Leu Ala Phe Val Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu
326 275 280 285
328 Asp Arg Gly Ala Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg
329 290 295 300
331 Leu Met Thr Gln Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp Ser
332 305 310 315 320
334 Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser
335 325 330 335
337 Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr
338 340 345 350

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VERIFICATION SUMMARY

DATE: 04/08/2002

PATENT APPLICATION: US/09/782,587B

TIME: 16:03:59

Input Set : A:\0213us310-SEQUENCE_LISTING-Nov2001.txt

Output Set: N:\CRF3\04082002\I782587B.raw

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:68 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1

L:71 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1

L:74 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1